

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising:
 - (a) a first nucleotide sequence encoding a first polypeptide having fructokinase activity, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:2, SEQ ID NO:6, or SEQ ID NO:12 have at least 80% identity based on the Clustal alignment method,
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 - (b) a second nucleotide sequence encoding a second polypeptide having fructokinase activity, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:8 or SEQ ID NO:10 have at least 90% identity based on the Clustal alignment method,
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 - (c) a third nucleotide sequence encoding a third polypeptide having fructokinase activity, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 95% identity based on the Clustal alignment method, or
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 - (d) the complement of the first, second, or third nucleotide sequence, wherein the complement and the first, second, or third nucleotide sequence contain the same number of nucleotides and are 100% complementary.
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2. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:2, SEQ ID NO:6, or SEQ ID NO:12 have at least 85% identity based on the Clustal alignment method.
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3. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:2, SEQ ID NO:6, or SEQ ID NO:12 have at least 90% identity based on the Clustal alignment method.
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4. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:2, SEQ ID NO:6, or SEQ ID NO:12 have at least 95% identity based on the Clustal alignment method, and wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:8 or SEQ ID NO:10 have at least 95% identity based on the Clustal alignment method.
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5. The polynucleotide of Claim 1, wherein the first polypeptide comprises the amino acid sequence of SEQ ID NO:2, SEQ ID NO:6, or SEQ ID NO:12, wherein the second polypeptide comprises the amino acid sequence of SEQ ID

NO:8 or SEQ ID NO:10, and wherein the third polypeptide comprises the amino acid sequence of SEQ ID NO:4.

6. The polynucleotide of Claim 1, wherein the first nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:5, or SEQ ID

5 NO:11, wherein the second nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:7 or SEQ ID NO:9, and wherein the third nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:3.

7. An vector comprising the polynucleotide of Claim 1.

8. A recombinant DNA construct comprising the polynucleotide of Claim 1 10 operably linked to a regulatory sequence.

9. A method for transforming a cell comprising transforming a cell with the polynucleotide of Claim 1.

10. A cell comprising the recombinant DNA construct of Claim 8.

11. A method for producing a plant comprising transforming a plant cell with the polynucleotide of Claim 1 and regenerating a plant from the transformed plant cell.

12. A plant comprising the recombinant DNA construct of Claim 8.

13. A seed comprising the recombinant DNA construct of Claim 8.

14. An isolated polynucleotide comprising a first nucleotide sequence,

20 wherein the first nucleotide sequence contains at least 30 nucleotides, and wherein the first nucleotide sequence is comprised by another polynucleotide, wherein the other polynucleotide includes:

25 (a) a second nucleotide sequence, wherein the second nucleotide sequence encodes a polypeptide having fructokinase activity, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:2, SEQ ID NO:6, or SEQ ID NO:12 have at least 80% sequence identity based on the Clustal alignment method, or

30 (b) the complement of the second nucleotide sequence, wherein the complement and the second nucleotide sequence contain the same number of nucleotides and are 100% complementary.

15. An isolated polynucleotide comprising a first nucleotide sequence, wherein the first nucleotide sequence contains at least 30 nucleotides, and wherein the first nucleotide sequence is comprised by another polynucleotide, wherein the other polynucleotide includes:

35 (a) a second nucleotide sequence, wherein the second nucleotide sequence encodes a polypeptide having fructokinase activity,

wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:8 or SEQ ID NO:10 have at least 90% sequence identity based on the Clustal alignment method, or

- 5 (b) the complement of the second nucleotide sequence, wherein the complement and the second nucleotide sequence contain the same number of nucleotides and are 100% complementary.

16. An isolated polynucleotide comprising a first nucleotide sequence, wherein the first nucleotide sequence contains at least 30 nucleotides, and wherein the first nucleotide sequence is comprised by another polynucleotide, wherein the 10 other polynucleotide includes:

- 15 (a) a second nucleotide sequence, wherein the second nucleotide sequence encodes a polypeptide having fructokinase activity, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 95% sequence identity based on the Clustal alignment method, or
- (b) the complement of the second nucleotide sequence, wherein the complement and the second nucleotide sequence contain the same number of nucleotides and are 100% complementary.

17. An isolated polypeptide having fructokinase activity wherein the 20 polypeptide comprises:

- 25 (a) a first amino acid sequence, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:2, SEQ ID NO:6, or SEQ ID NO:12 have at least 80% identity based on the Clustal alignment,
- (b) a second amino acid sequence, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:8 or SEQ ID NO:10 have at least 90% identity based on the Clustal alignment method, or
- 30 (c) a third amino acid sequence, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:4 have at least 95% identity based on the Clustal alignment method.

18. The polypeptide of Claim 17, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:2, SEQ ID NO:6, or SEQ ID NO:12 have at least 85% identity based on the Clustal alignment method.

35 19. The polypeptide of Claim 17, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:2, SEQ ID NO:6, or SEQ ID NO:12 have at least 90% identity based on the Clustal alignment method.

20. The polypeptide of Claim 17, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:2, SEQ ID NO:6, or SEQ ID NO:12 have at least 95% identity based on the Clustal alignment method, and wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:8 or SEQ ID NO:10 have at least 95% identity based on the Clustal alignment method.

5 21. The polypeptide of Claim 17, wherein the first amino acid comprises the amino acid sequence of SEQ ID NO: 2, SEQ ID NO:6, or SEQ ID NO:12, wherein the second amino acid sequence comprises the amino acid sequence of SEQ ID NO:8 or SEQ ID NO:10, and wherein the third amino acid comprises the amino acid sequence of SEQ ID NO:4.

10 22. A method for isolating a polypeptide encoded by the polynucleotide of Claim 1 comprising isolating the polypeptide from a cell containing a recombinant DNA construct comprising the polynucleotide operably linked to a regulatory sequence.

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